

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 09/996,620
Source: IFW 16
Date Processed by STIC: 11-16-2004.

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 11/16/2004

PATENT APPLICATION: US/09/996,620

TIME: 13:34:57

Input Set : N:\FANTU\US09996620.raw

Output Set: N:\CRF4\11162004\I996620.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:

2 (i) APPLICANT: Boodhoo, Amechand

3 Seehra, Jasbir

4 Shaw, Gray

5 Sako, Dianne

6 (ii) TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM

7 PROTEASE, POLYNUCLEOTIDES ENCODING SAME AND RELATED

PROTEASES, AND

8 THERAPEUTIC USES THEREOF

9 (iii) NUMBER OF SEQUENCES: 22

10 (iv) CORRESPONDENCE ADDRESS:

11 (A) ADDRESSEE: Genetics Institute, Inc.

12 (B) STREET: 87 CambridgePark Drive

13 (C) CITY: Cambridge

14 (D) STATE: Massachusetts

15 (E) COUNTRY: USA

16 (F) ZIP: 02140

17 (v) COMPUTER READABLE FORM:

18 (A) MEDIUM TYPE: Floppy disk

19 (B) COMPUTER: IBM PC compatible

20 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

21 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

22 (vi) CURRENT APPLICATION DATA:

C--> 23 (A) APPLICATION NUMBER: US/09/996,620

C--> 24 (B) FILING DATE: 27-Nov-2001

25 (C) CLASSIFICATION:

26 (vii) PRIOR APPLICATION DATA:

27 (A) APPLICATION NUMBER: 09/026,001

28 (B) FILING DATE: 18-FEB-1998

29 (viii) ATTORNEY/AGENT INFORMATION:

30 (A) NAME: Brown, Scott A.

31 (B) REGISTRATION NUMBER: 32,724

32 (C) REFERENCE/DOCKET NUMBER: GI5293B

33 (ix) TELECOMMUNICATION INFORMATION:

34 (A) TELEPHONE: (617) 498-8224

35 (B) TELEFAX: (617) 876-5851

36 (2) INFORMATION FOR SEQ ID NO: 1:

37 (i) SEQUENCE CHARACTERISTICS:

38 (A) LENGTH: 30 amino acids

39 (B) TYPE: amino acid

40 (C) STRANDEDNESS: single

41 (D) TOPOLOGY: linear

42 (ii) MOLECULE TYPE: peptide

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43 (iii) HYPOTHETICAL: NO
44 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
45 Thr Asn Thr Pro Glu Gln Asp Arg Tyr Leu Gln Ala Lys Lys Tyr Ile
46 1 5 10 15
47 Glu Phe Tyr Val Val Val Asp Asn Val Met Tyr Arg Lys Tyr
48 20 25 30
50 (2) INFORMATION FOR SEQ ID NO: 2:
51 (i) SEQUENCE CHARACTERISTICS:
52 (A) LENGTH: 48 amino acids
53 (B) TYPE: amino acid
54 (C) STRANDEDNESS: single
55 (D) TOPOLOGY: linear
56 (ii) MOLECULE TYPE: peptide
57 (iii) HYPOTHETICAL: NO
58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
59 Thr Asn Thr Pro Glu Gln Asp Arg Tyr Leu Gln Ala Lys Lys Tyr Ile
60 1 5 10 15
61 Glu Phe Tyr Val Val Val Asp Asn Val Met Tyr Arg Lys Tyr Thr Gly
62 20 25 30
W--> 63 Lys Leu His Val Ile Thr Xaa Xaa Val Tyr Glu Met Asn Ala Leu Asn
64 35 40 45
66 (2) INFORMATION FOR SEQ ID NO: 3:
67 (i) SEQUENCE CHARACTERISTICS:
68 (A) LENGTH: 15 amino acids
69 (B) TYPE: amino acid
70 (C) STRANDEDNESS: single
71 (D) TOPOLOGY: linear
72 (ii) MOLECULE TYPE: peptide
73 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
74 Glu Ala Thr Glu Tyr Glu Tyr Leu Asp Tyr Asp Phe Leu Pro Glu
75 1 5 10 15
77 (2) INFORMATION FOR SEQ ID NO: 4:
78 (i) SEQUENCE CHARACTERISTICS:
79 (A) LENGTH: 15 amino acids
80 (B) TYPE: amino acid
81 (C) STRANDEDNESS: single
82 (D) TOPOLOGY: linear
83 (ii) MOLECULE TYPE: peptide
84 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
85 Gln Ala Thr Glu Tyr Glu Tyr Leu Asp Tyr Asp Phe Leu Pro Glu
86 1 5 10 15
88 (2) INFORMATION FOR SEQ ID NO: 5:
89 (i) SEQUENCE CHARACTERISTICS:
90 (A) LENGTH: 2050 base pairs
91 (B) TYPE: nucleic acid
92 (C) STRANDEDNESS: double
93 (D) TOPOLOGY: linear
94 (ii) MOLECULE TYPE: cDNA
95 (ix) FEATURE:

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96      (A) NAME/KEY: CDS
97      (B) LOCATION: 78..1940
98      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
99 AGTCAATAGG AGAAGAGCTC AGGTTGGCTT GGAAGCAGAA AGAGATTCCT GTCCACCACT      60
100 CCAATCCAGG CTCCAAATG ATCCAAGCTC TCTTGGTAGC TATATGCTTA GCGGTTTTTC      120
101 CATATCAAGG GAGCTCTATA ATCCTGGAAT CCGGGAATGT TAATGATTAT GAAGTAGTGT      180
102 ATCCACAAAA AGTGCCTGCA TTGTCCAAAG GAGGAGTTCA GAATCCTCAG CCAGAGACCA      240
103 AGTATGAAGA TACAATGCAA TATGAATTTT ACGTGAACGG AGAGCCAGTG GTCCTTCACT      300
104 TAGAAAGAAA TAAAGGACTT TTTTCAGAAG ATTACACTGA AACTCATTAT GCCCCTGATG      360
105 GCAGAGAAAT TACAACAAGC TCTCCAGTTC AGGATCACTG CTATTATCAT GGTACATTC      420
106 AGAATGAAGC TGACTCAAGT GCAGTCATCA GTGCATGTGA TGGCTTGAAA GGACATTTCA      480
107 AGCATCAAGG GGAGACATAC TTTATTGAGC CTTTGGAGCT TTCTGACAGT GAAGCCCATG      540
108 CAATATACAA AGATGAAAAT GTAGAAGAAG AGGAAGAGAT CCCCAAAATC TGTGGGGTTA      600
109 CCCAGACTAC TTGGGAATCA GATGAGCCGA TTGAAAAGTC CTCTCAGTTA ACTAATACTC      660
110 CTGAACAAGA CAGGTACTTG CAGGCCAAAA AATACATCGA GTTTTACGTG GTTGTGGACA      720
111 ATGTAATGTA CMGRAAATAC ACCGGCAAGT TACATGTTAT AACAGAAGA GTATATGAAA      780
112 TGGTCAACGC TTAAATACG ATGTACAGAC GTTTGAATTT TCACATAGCA CTGATTGGCC      840
113 TAGAAATTTG GTCCAACGGA AATGAGATTA ATGTGCAATC AGACGTGCAG GCCACTTTGG      900
114 ACTTATTTGG AGAATGGAGA GAAAATAAAT TGCTGCCACG CAAAAGGAAT GATAATGCTC      960
115 AGTTACTCAC GAGCACTGAG TTCAATGGAA CTACTACAGG ACTTGGTTAC ATAGGCTCCC      1020
116 TCTGTAGTCC GAAGAAATCT GTGGCAGTTG TTCAGGATCA TAGCAAAAGC ACAAGCATGG      1080
117 TGGCAATTAC AATGGCCCAT CAGATGGGTC ATAATCTGGG CATGAATGAT GACAGAGCTT      1140
118 CCTGTACTTG TGGTTCTAAC AAATGCATTA TGTCTACAAA ATATTATGAA TCTCTTTCTG      1200
119 AGTTCAGCTC TTGTAGTGTC CAGGAACATC GGGAGTATCT TCTTAGAGAC AGACCACAAT      1260
120 GCATTCTCAA CAAACCCTCG CGCAAAGCTA TTGTTACACC TCCAGTTTGT GGAAATTACT      1320
121 TTGTGGAGCG GGGAGAAGAA TGTGACTGTG GCTCTCCTGA GGATTGTCAA AATACCTGCT      1380
122 GTGATGCTGC AACTTGTAAG CTGCAACATG AGGCACAGTG TGACTCTGGA GAGTGTGTGT      1440
123 AGAAATGCAA ATTTAAGGGA GCAGGAGCAG AATGCCGGGC AGCAAAGAAT GACTGTGACT      1500
124 TTCCTGAAC CTGCACTGGC CGATCTGCTA AGTGTCCCAA GGACAGCTTC CAGAGGAATG      1560
125 GACATCCATG CCAAAACAAC CAAGGTACTT GCTACAATGG GACATGTCCC ACCTTGACAA      1620
126 ACCAATGTGC TACTCTCTGG GGGCCAGGTG CAAAATATGT TCCAGGTTTA TGTTTTATGT      1680
127 TGAAGTGGAA TGCCCGAAGT TGTGGCTTGT GCAGAAAGGA AAATGGCAGA AAGATTCTAT      1740
128 GTGCAGCAAA GGATGTAAAG TGTGGCAGGT TATTTTGTCAA AAAGAAAAAC TCGATGATAT      1800
129 GCCACTGCCC ACTCCATCAA AGGACCCAAA TTATGGAATG GTTGACCTG GAACAAAATG      1860
130 TGGAGTTAAA AAGGTGTGCA GAAACAGGCA ATGTGTAAA GTATAGACAG CCAACTGATC      1920
131 AAGCACTGCT TCTCTCAATT TGATTTTGGG GATCCTCCTT CCAGAAGGCT TTCCTCAAGT      1980
132 CCAAAGAGAC CCATCTGTCT TTATCCTACT AGTAAATCAC TCTTAGCTTT CAAAAAATA      2040
133 AAAAGTCGAC                                     2050
135 (2) INFORMATION FOR SEQ ID NO: 6:
136      (i) SEQUENCE CHARACTERISTICS:
137          (A) LENGTH: 621 amino acids
138          (B) TYPE: amino acid
139          (C) STRANDEDNESS:
140          (D) TOPOLOGY: linear
141      (ii) MOLECULE TYPE: protein
142      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
143      Met Ile Gln Ala Leu Leu Val Ala Ile Cys Leu Ala Val Phe Pro Tyr
144      1             5             10             15
145      Gln Gly Ser Ser Ile Ile Leu Glu Ser Gly Asn Val Asn Asp Tyr Glu

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146		20		25		30								
147	Val	Val	Tyr	Pro	Gln	Lys	Val	Pro	Ala	Leu	Ser	Lys	Gly	Gly
148		35					40					45		
149	Asn	Pro	Gln	Pro	Glu	Thr	Lys	Tyr	Glu	Asp	Thr	Met	Gln	Tyr
150		50				55						60		
151	His	Val	Asn	Gly	Glu	Pro	Val	Val	Leu	His	Leu	Glu	Arg	Asn
152		65				70				75				80
153	Leu	Phe	Ser	Glu	Asp	Tyr	Thr	Glu	Thr	His	Tyr	Ala	Pro	Asp
154				85					90					95
155	Glu	Ile	Thr	Thr	Ser	Ser	Pro	Val	Gln	Asp	His	Cys	Tyr	Tyr
156				100					105					110
157	Tyr	Ile	Gln	Asn	Glu	Ala	Asp	Ser	Ser	Ala	Val	Ile	Ser	Ala
158			115						120				125	
159	Gly	Leu	Lys	Gly	His	Phe	Lys	His	Gln	Gly	Glu	Thr	Tyr	Phe
160		130					135					140		
161	Pro	Leu	Glu	Leu	Ser	Asp	Ser	Glu	Ala	His	Ala	Ile	Tyr	Lys
162		145				150					155			160
163	Asn	Val	Glu	Glu	Glu	Glu	Glu	Ile	Pro	Lys	Ile	Cys	Gly	Val
164				165						170				175
165	Thr	Thr	Trp	Glu	Ser	Asp	Glu	Pro	Ile	Glu	Lys	Ser	Ser	Gln
166			180						185					190
167	Asn	Thr	Pro	Glu	Gln	Asp	Arg	Tyr	Leu	Gln	Ala	Lys	Lys	Tyr
168			195					200					205	
169	Phe	Tyr	Val	Val	Val	Asp	Asn	Val	Met	Tyr	Arg	Lys	Tyr	Thr
170		210					215					220		
171	Leu	His	Val	Ile	Thr	Arg	Arg	Val	Tyr	Glu	Met	Val	Asn	Ala
172		225				230					235			240
173	Thr	Met	Tyr	Arg	Arg	Leu	Asn	Phe	His	Ile	Ala	Leu	Ile	Gly
174				245					250					255
175	Ile	Trp	Ser	Asn	Gly	Asn	Glu	Ile	Asn	Val	Gln	Ser	Asp	Val
176			260					265					270	
177	Thr	Leu	Asp	Leu	Phe	Gly	Glu	Trp	Arg	Glu	Asn	Lys	Leu	Leu
178		275					280						285	
179	Lys	Arg	Asn	Asp	Asn	Ala	Gln	Leu	Leu	Thr	Ser	Thr	Glu	Phe
180		290					295				300			
181	Thr	Thr	Thr	Gly	Leu	Gly	Tyr	Ile	Gly	Ser	Leu	Cys	Ser	Pro
182		305				310					315			320
183	Ser	Val	Ala	Val	Val	Gln	Asp	His	Ser	Lys	Ser	Thr	Ser	Met
184				325					330					335
185	Ile	Thr	Met	Ala	His	Gln	Met	Gly	His	Asn	Leu	Gly	Met	Asn
186			340						345				350	
187	Arg	Ala	Ser	Cys	Thr	Cys	Gly	Ser	Asn	Lys	Cys	Ile	Met	Ser
188			355					360					365	
189	Tyr	Tyr	Glu	Ser	Leu	Ser	Glu	Phe	Ser	Ser	Cys	Ser	Val	Gln
190		370					375					380		
191	Arg	Glu	Tyr	Leu	Leu	Arg	Asp	Arg	Pro	Gln	Cys	Ile	Leu	Asn
192		385				390					395			400
193	Ser	Arg	Lys	Ala	Ile	Val	Thr	Pro	Pro	Val	Cys	Gly	Asn	Tyr
194				405					410					415

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195   Glu Arg Gly Glu Glu Cys Asp Cys Gly Ser Pro Glu Asp Cys Gln Asn
196                               420                     425                     430
197   Thr Cys Cys Asp Ala Ala Thr Cys Lys Leu Gln His Glu Ala Gln Cys
198                               435                     440                     445
199   Asp Ser Gly Glu Cys Cys Glu Lys Cys Lys Phe Lys Gly Ala Gly Ala
200                               450                     455                     460
201   Glu Cys Arg Ala Ala Lys Asn Asp Cys Asp Phe Pro Glu Leu Cys Thr
202   465                               470                     475                     480
203   Gly Arg Ser Ala Lys Cys Pro Lys Asp Ser Phe Gln Arg Asn Gly His
204                               485                     490                     495
205   Pro Cys Gln Asn Asn Gln Gly Tyr Cys Tyr Asn Gly Thr Cys Pro Thr
206                               500                     505                     510
207   Leu Thr Asn Gln Cys Ala Thr Leu Trp Gly Pro Gly Ala Lys Met Ser
208                               515                     520                     525
209   Pro Gly Leu Cys Phe Met Leu Asn Trp Asn Ala Arg Ser Cys Gly Leu
210                               530                     535                     540
211   Cys Arg Lys Glu Asn Gly Arg Lys Ile Leu Cys Ala Ala Lys Asp Val
212   545                               550                     555                     560
213   Lys Cys Gly Arg Leu Phe Cys Lys Lys Lys Asn Ser Met Ile Cys His
214                               565                     570                     575
215   Cys Pro Leu His Gln Arg Thr Gln Ile Met Glu Trp Leu His Leu Glu
216                               580                     585                     590
217   Gln Asn Val Glu Leu Lys Arg Cys Ala Glu Thr Gly Asn Val Leu Lys
218   595                               600                     605
219   Tyr Arg Gln Pro Thr Asp Gln Ala Leu Leu Leu Ser Ile
220   610                               615                     620

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222 (2) INFORMATION FOR SEQ ID NO: 7:

223 (i) SEQUENCE CHARACTERISTICS:

224 (A) LENGTH: 2297 base pairs

225 (B) TYPE: nucleic acid

226 (C) STRANDEDNESS: double

227 (D) TOPOLOGY: linear

228 (ii) MOLECULE TYPE: cDNA

229 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```

230 GTCGACCAGT CAACAGGAGA AAAGCTCAGG TTGGCTTGGA AGCAGAAAGA GATTCCTGTC      60
231 CACCAGTCCA ATCCAGGCTC CAAAATGATC CAAGCTCTCT TGGTAATTAT ATGCTTAGCG      120
232 GTTTTTCAT ATCAAGGGAG CTCTATAATC CTGGAATCTG GGAATGTTAA TGATTATGAA      180
233 GTTGTGTATC CACAAAAGT GCCTGCATTG CTCAAAGGAG GAGTTCAGAA TCCTCAGCCA      240
234 GAGACCAAGT ATGAAGATAC AATGCAATAT GAATTTCAAG TGAATGGAGA GCCAGTAGTC      300
235 CTTCACTTAG AAAGAAATAA AGGACTTTTT TCAGAAGATT AACTGAAAC TCATTATGCC      360
236 CCTGATGGCA GAGAAATTAC AACAGCCCT CCGGTTTCAGG ATCACTGCTA TTATCATGGT      420
237 TACATTGAGA ATGAAGCTGA CTCAAGTGCA ATCATCAGTG CATGTGATGG CTTGAAAGGA      480
238 CATTTCAAGC ATCAAGGGGA GACATACTTT ATTGAGCCCT TGAAGCTTTT CGACAGTGAA      540
239 TCTCATGCAA TCTACAAAGA TGAAAATGTA GAAAACGAGG ATGAGACCCC CGAAACCTGT      600
240 GGGGTAACCG AGACTACTTG GGAGTCAGAT GAGTCCATCG AAAAGACCTC TCAGTTAACT      660
241 AACACTCCTG AACAGACGG GTACTTGCAG GCCAAAAAAT ACATCGAGTT TTACGTGGTT      720
242 GTGGACAACA GAATGTACAG GTATTACAAA CGCAATGAAC CTGCTATAAA AAGAAGAGTA      780
243 TATGAAATGG TCAACGCTGT AAATACGAAG TACAGACCTT TGAAAATTCA CATAACACTG      840
244 ATTGGCCTAG AAATTTGGTC CAACCATGAT AAGTTTGAAG TGAAGCCAGT AGCGGGTGCC      900

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VERIFICATION SUMMARY

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TIME: 13:34:58

Input Set : N:\FANTU\US09996620.raw

Output Set: N:\CRF4\11162004\I996620.raw

:23 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
:24 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
:63 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:32